



# 4

## SEQUENCE LISTING

<110> Goldman, Stanley  
Lathrop, Stephanie J.  
Longchamp, Pascal F.  
Whalen, Robert G.  
Maxygen, Inc.

<120> Methods and Compositions for Developing Spore Display  
Systems for Medicinal and Industrial Applications

<130> 18097A-033520US

<140> US 10/028,247

<141> 2001-12-19

<150> US 60/214,161

<151> 2000-06-26

<150> US 09/892,208

<151> 2001-06-26

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 258

<212> DNA

<213> Bacillus subtilis

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<221> CDS

<222> (1)..(258)

<223> CotC27 including HA11 epitope region

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acg	tat	tat	aag	aag	tat	tac	gaa	tat	gat	aaa	tct	aga	ggt	acc	tgc	96
Thr	Tyr	Tyr	Lys	Lys	Tyr	Tyr	Glu	Tyr	Asp	Lys	Ser	Arg	Gly	Thr	Cys	
			20				25						30			

tat	cct	tat	gat	gtt	cct	gat	tat	gct	tct	tta	gga	tcc	ctg	cag	aaa	144
Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser	Leu	Gly	Ser	Leu	Gln	Lys	
			35				40					45				

gat	tat	gac	tgt	gat	tac	gac	aaa	aaa	tat	gat	gac	tat	gat	aaa	aaa	192
Asp	Tyr	Asp	Cys	Asp	Tyr	Asp	Lys	Lys	Tyr	Asp	Asp	Tyr	Asp	Lys	Lys	
			50				55				60					

tat	tat	gat	cac	gat	aaa	aaa	gac	tat	gat	tat	gtt	gta	gag	tat	aaa	240
Tyr	Tyr	Asp	His	Asp	Lys	Lys	Asp	Tyr	Asp	Tyr	Val	Val	Glu	Tyr	Lys	
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Lys	His	Lys	Lys	His	Tyr											
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 <213> Bacillus subtilis

<220>  
 <223> CotC27 including HA11 epitope region

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 20 25 30  
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Leu Gln Lys  
 35 40 45  
 Asp Tyr Asp Cys Asp Tyr Asp Lys Lys Tyr Asp Asp Tyr Asp Lys Lys  
 50 55 60  
 Tyr Tyr Asp His Asp Lys Lys Asp Tyr Asp Tyr Val Val Glu Tyr Lys  
 65 70 75 80  
 Lys His Lys Lys His Tyr  
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<210> 3  
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 1 5 10 15  
 ctg tca gtc aca tcg ctg ttt gcg atg cag ccg tca gca aaa gcc gct 96  
 Leu Ser Val Thr Ser Leu Phe Ala Met Gln Pro Ser Ala Lys Ala Ala  
 20 25 30  
 gaa cac aat cca gtt gtt atg gtt cac ggt atc gga gga gct tca tac 144  
 Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr  
 35 40 45  
 aat ttt gcg gga att aag agc tat ctc gta tct cag gcc tgg tca cgg 192  
 Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg  
 50 55 60  
 ggc aag ctg tat gcg gtt gat ttt tgg gac aag aca ggg acg aat tat 240  
 Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr  
 65 70 75 80  
 aac aat ggc ccg gta tta tca cga ttt gtg caa aag gtt tta gac gaa 288  
 Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu  
 85 90 95  
 acg ggt gcg aaa aaa gtg gat att gtc gct cac agc atg ggt ggc gcg 336  
 Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala  
 100 105 110

aac aca ctt tac tac ata aaa aat ctg gac ggc gga aat aaa att gaa	384
Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu	
115 120 125	
aac gtc gta acg ctt ggc ggc gcg aac cgt ttg acg aca agc aag gcg	432
Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala	
130 135 140	
ctt ccg gga aca gat cca aat caa aag att tta tac aca tcc att tac	480
Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr	
145 150 155 160	
agc agt gcc gat atg att gtc atg aat tac tta tca aaa tta gac ggt	528
Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly	
165 170 175	
gct aaa aac gtt caa att cat ggc gtt ggg cac att ggt tta ttg atg	576
Ala Lys Asn Val Gln Ile His Gly Val Gly His Ile Gly Leu Leu Met	
180 185 190	
aac agc caa gtc aac agc ctg att aaa gaa gga ctg aac ggc ggg ggc	624
Asn Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly Gly	
195 200 205	
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Leu Asn Thr Asn	
210	

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<220>  
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<400> 4

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Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr	
35 40 45	
Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg	
50 55 60	
Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr	
65 70 75 80	
Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu	
85 90 95	
Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala	
100 105 110	
Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu	
115 120 125	
Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala	
130 135 140	
Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr	
145 150 155 160	
Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly	
165 170 175	

Ala	Lys	Asn	Val	Gln	Ile	His	Gly	Val	Gly	His	Ile	Gly	Leu	Leu	Met
			180					185					190		
Asn	Ser	Gln	Val	Asn	Ser	Leu	Ile	Lys	Glu	Gly	Leu	Asn	Gly	Gly	Gly
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Leu	Asn	Thr	Asn												
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 <213> Artificial Sequence

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<210> 6  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer for  
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32